**BIOTECHNOLOGY
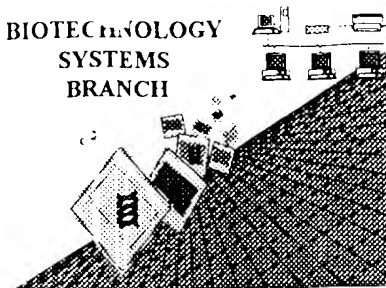SYSTEMS
BRANCH**

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/923,844_

Source: _OIPE_

Date Processed by STIC: _8/16/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

OIPE

RAW SEQUENCE LISTING   DATE: 08/16/2001
PATENT APPLICATION: **US/09/923,844**   TIME: 12:54:02

Input Set : **A:\Seqlist.txt**
Output Set: **N:\CRF3\08162001\I923844.raw**

Does Not Comply
Corrected Diskette Needed

```
   4 <110> APPLICANT: Bao, Zhongmeng
   5         Lu, Guihua
   7 <120> TITLE OF INVENTION: Sclerotinia-inducible Genes and
   8         Promoters and Their Uses
  10 <130> FILE REFERENCE: 35718/234631
```
C--> 12 **<140> CURRENT APPLICATION NUMBER: US/09/923,844**
C--> 12 **<141> CURRENT FILING DATE: 2001-08-07**
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  12 <150> PRIOR APPLICATION NUMBER: US 60/224,603
  13 <151> PRIOR FILING DATE: 2000-08-11
  15 <160> NUMBER OF SEQ ID NOS: 20
  17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

ERRORED SEQUENCES

sie p. 4

```
 128 <210> SEQ ID NO: 2
 129 <211> LENGTH: 371
 130 <212> TYPE: PRT
 131 <213> ORGANISM: Helianthus annuus
 133 <400> SEQUENCE: 2
 134 Met Glu Phe Leu Lys Ala Pro Thr Leu Leu Leu Val Ile Phe Ser Leu
 135 1               5                   10                  15
 136 Ala Ile Cys Ser Pro Ile Ser Ala Gln Asn Lys Gly Gly Tyr Trp Pro
 137             20                  25                  30
 138 Ser Trp Ala Gln Asp Phe Leu Pro Pro Ser Asn Ile Gln Thr Ala Tyr
 139         35                  40                  45
 140 Phe Thr His Val Tyr Tyr Ala Phe Leu Ser Pro Asn Asn Val Thr Phe
 141     50                  55                  60
 142 Gln Phe Asp Val His Arg Thr Thr Ala Ser Ala Leu Asn Ser Phe Asn
 143 65                  70                  75                  80
 144 Thr Ala Leu His Gly Lys Asn Pro Pro Val Lys Thr Leu Phe Ser Ile
 145                 85                  90                  95
 146 Gly Gly Gly Ser Ala Gly Val Lys Gln Leu Phe Ser Lys Leu Ala Ser
 147             100                 105                 110
 148 Ser Pro Gly Ser Arg Ala Ala Phe Ile Arg Ser Thr Ile Gln Val Ala
 149         115                 120                 125
 150 Arg Asn Tyr Tyr Phe Asp Gly Ala Asp Leu Asp Trp Glu Tyr Pro Glu
 151     130                 135                 140
 152 Thr Gln Thr Asp Met Asn Asn Phe Gly Leu Leu Leu Asp Glu Trp Arg
 153 145                 150                 155                 160
 154 Val Ala Val Asn Asn Glu Ala Thr Ser Thr Gly Lys Pro Arg Leu Leu
 155                 165                 170                 175
 156 Leu Ser Ala Ala Thr Arg His Glu Pro Glu Val Arg Asp Asn Gly Val
 157             180                 185                 190
 158 Ala Lys Tyr Pro Val Ala Ser Ile Asn Lys Asn Leu Asp Gly Ile Asn
 159         195                 200                 205
 160 Ala Met Cys Tyr Asp Tyr His Gly Pro Trp Thr Pro Asp Ala Thr Gly
```

```
161     210                     215                     220
162 Ala Pro Ala Ala Leu Tyr Asn Pro Asn Gly Ser Leu Ser Thr Ser Asn
163 225                     230                     235                     240
164 Gly Leu Gln Ser Trp Ile Ser Ala Gly Ile Gln Arg Gln Lys Leu Val
165                     245                     250                     255
166 Met Gly Met Pro Leu Tyr Gly Trp Thr Trp Lys Leu Lys Asn Pro Ser
167                     260                     265                     270
168 Val Asn Gly Ile Gly Ala Pro Ala Ala Gly Ile Gly Pro Gly Asn Glu
169             275                     280                     285
170 Gly Ala Met Leu Tyr Ser Glu Val Gln Gln Phe Asn Ala Gln Asn Asn
171         290                     295                     300
172 Ala Arg Val Val Tyr Asp Thr Gln Thr Val Ser Tyr Tyr Ser Tyr Ser
173 305                     310                     315                     320
174 Gly Thr Thr Trp Ile Gly Tyr Asp Asp Val Asn Ser Val Gln Arg Lys
175                     325                     330                     335
176 Val Gln Tyr Ala Lys Ser Leu Asn Ile Gly Gly Tyr Phe Phe Trp Thr
```

E--> 177

```
        340                 345                 350      Ala Val Gly Asp Gln Asp Trp Lys
221 <210> SEQ ID NO: 4
222 <211> LENGTH: 97
223 <212> TYPE: PRT
224 <213> ORGANISM: Helianthus annuus
226 <400> SEQUENCE: 4
227 Met Lys Ala Pro Thr Met Ile Cys Phe Leu Val Ala Val Ile Ala Ala
228 1               5                   10                  15
229 Met Met Val Phe Met Gly Gln Leu Pro Ala Ala Thr Ala Val Thr Cys
230         20                  25                  30
231 Asn Tyr Met Glu Leu Val Pro Cys Ala Gly Ala Ile Ser Ser Ser Gln
232         35                  40                  45
233 Pro Pro Ser Gly Ser Cys Cys Ser Lys Val Arg Glu Gln Arg Pro Cys
234     50                  55                  60
235 Phe Cys Gly Tyr Leu Arg Asn Pro Ser Leu Arg Gln Phe Val Ser Pro
```

E--> 236

```
65                  70                  75              80  Ala Ala Ala Gln Lys Ile Ala Ser
238 <210> SEQ ID NO: 5
239 <211> LENGTH: 849
240 <212> TYPE: DNA
241 <213> ORGANISM: Helianthus annuus
243 <400> SEQUENCE: 5
244 cgtcgtttcg cttgcagggg gataaaagat aatatcatga tcaccattca tcacgcctaa          60
245 aattcctcct cttagtcaat tgtgaatatt ttgtaattat tgtgtagact ataactgtta         120
246 tgtctttgca tatatttctc cttgtaatta gccttgtatt ccagtatata atgatatcaa         180
247 aactctctaa tcaagcagag agagttccct gaattacatc accgctgcca ttttagtcca         240
248 ctaagttaac ttcatccatt aattttgtta acgtgaaagg aaattcggtc attttctatg         300
249 gccgaattgc ccttgtagtt cacaaaatta catataaaac caccgaattg ccgttctcgt         360
250 taacagaaaa aatgaatgaa gttaacccag tggactaaaa tygcaacgat gaaaccattt         420
251 tggatccaca ggcgaaaaat gaaacttttg gactaaactg gcgaaaaata aaacttttgg         480
252 actaaactac atgaactaaa atggctttta actaaatttt aataaccgtt ttaattttat         540
253 aaagagaaaa taaactttac aaaaagcatc gcttgtctat tttataaaga ttaaagttac         600
254 ttgcacgttc aaacatatgt tactagatga atcaagagtc atgtacaact ctatgtttag         660
255 ataaggttac tagatgaata tgagttagtc atctataagt ctatacttag aaagttcaaa         720
```

```
RAW SEQUENCE LISTING                    DATE: 08/16/2001
PATENT APPLICATION:  US/09/923,844      TIME: 12:54:02

        Input Set : A:\Seqlist.txt
        Output Set: N:\CRF3\08162001\I923844.raw
```

```
E--> 256
gtcaatgatt tgtattgaat actgtttgta gttgaattca taaaagcttt gaatactgtt       780tgtagttgaa ttcataaaag
                                                                           ↑
     258 <210> SEQ ID NO: 6
     259 <211> LENGTH: 1089
     260 <212> TYPE: DNA
     261 <213> ORGANISM: Helianthus annuus
     263 <400> SEQUENCE: 6
     264 atcctactac ctcaaacttt atctaattca tcaacacaac ggaggtttgg ttatatttgt        60
     265 ttggtccatc caaaaggaca aaaatgcact tcatcttaac aaaaaaaaaa aaaaaaaaaa       120
     266 ctaagttagt gatttggatg aaaatgacaa acaaaaggac aaaaatgcac ttcatcttaa       180
     267 caaaaaaaaa actgagttag taatttggat gaaaacgaca aaaaaagaca aacctgaaag       240
     268 attcaaatgc acaaaaaaat tattttggat gaaacacgca tatatgatca aacccaagag       300
     269 acgattttaa tattttactc gaaattttaa aagaagttaa tattagacag gaatcatgtt       360
     270 agagacatat gccaaaccta ttaattttct aagttcaaac aaaaatctat tattttttcc       420
     271 aaaccacagc tataatttat gtaattttat ctctataaat ggacaaagaa taaaagtttt       480
     272 ctacaaacgg taacaacaag gaagctaccc tcgttttgaa gatagttaag acaataattc       540
     273 aactactttc taactacttt tctcacaaga cttaattttc cacacacatc tttatgacta       600
     274 aatctaccat atgtgatggg ccagtcaacc attaatatgt cttcaaccac aagtcggtaa       660
     275 accggaccat cagccacttg gccacgggcg cagcttagtg gaaaccgggg gtgcacaacc       720
     276 cctctaatgt ttcggttaga agtgcaaaat ttacgatttt tcgtccgaaa attttcgccc       780
     277 accagaactt ttagtcaaac ttcgccactg cactttgccc aatgttctat taaggttttt       840
     278 attttatttt tattattttt tataacgatt ccaaaaattt tttggacata tacatctgac       900
     279 atgcgttata tgtagatata gaatttgaac tcgcaacctt ttaattatac gatacatcac       960
E--> 280
cacctagatt tgaattctca ttgggcccaa tggtctataa ataatgcacc aacccctcag      1020tttaaaccac caccactaca
                                                                           ↑
```

<210> 2
<211> 371
<212> PRT
<213> Helianthus annuus

<400> 2
Met Glu Phe Leu Lys Ala Pro Thr Leu Leu Leu Val Ile Phe Ser Leu 1
5   10   15 Ala Ile Cys Ser Pro Ile Ser Ala
Gln Asn Lys Gly Gly Tyr Trp Pro   20   25
30   Ser Trp Ala Gln Asp Phe Leu Pro Pro Ser Asn Ile Gln Thr Ala Tyr
35   40   45   Phe Thr His Val Tyr Tyr
Ala Phe Leu Ser Pro Asn Asn Val Thr Phe   50   55
60   Gln Phe Asp Val His Arg Thr Thr Ala Ser Ala Leu Asn Ser Phe
Asn65   70   75   80   Thr Ala Leu
His Gly Lys Asn Pro Pro Val Lys Thr Leu Phe Ser Ile   85
90   95   Gly Gly Gly Ser Ala Gly Val Lys Gln Leu Phe Ser Lys
Leu Ala Ser   100   105   110   Ser
Pro Gly Ser Arg Ala Ala Phe Ile Arg Ser Thr Ile Gln Val Ala   115
120   125   Arg Asn Tyr Tyr Phe Asp Gly Ala Asp Leu Asp
Trp Glu Tyr Pro Glu   130   135   140
Thr Gln Thr Asp Met Asn Asn Phe Gly Leu Leu Leu Asp Glu Trp Arg145
150   155   160 Val Ala Val Asn Asn Glu Ala Thr Ser
Thr Gly Lys Pro Arg Leu Leu   165   170
175   Leu Ser Ala Ala Thr Arg His Glu Pro Glu Val Arg Asp Asn Gly Val
180   185   190   Ala Lys Tyr Pro Val Ala Ser
Ile Asn Lys Asn Leu Asp Gly Ile Asn   195   200
205   Ala Met Cys Tyr Asp Tyr His Gly Pro Trp Thr Pro Asp Ala Thr Gly
210   215   220   Ala Pro Ala Ala Leu
Tyr Asn Pro Asn Gly Ser Leu Ser Thr Ser Asn225   230
235   240 Gly Leu Gln Ser Trp Ile Ser Ala Gly Ile Gln Arg Gln Lys
Leu Val   245   250   255   Met Gly
Met Pro Leu Tyr Gly Trp Thr Trp Lys Leu Lys Asn Pro Ser   260
265   270   Val Asn Gly Ile Gly Ala Pro Ala Ala Gly Ile Gly
Pro Gly Asn Glu   275   280   285
Gly Ala Met Leu Tyr Ser Glu Val Gln Gln Phe Asn Ala Gln Asn Asn   290
295   300   Ala Arg Val Val Tyr Asp Thr Gln Thr Val
Ser Tyr Tyr Ser Tyr Ser305   310   315
320 Gly Thr Thr Trp Ile Gly Tyr Asp Asp Val Asn Ser Val Gln Arg Lys
325   330   335   Val Gln Tyr Ala Lys Ser Leu Asn
Ile Gly Gly Tyr Phe Phe Trp Thr   340   345
350   Ala Val Gly Asp Gln Asp Trp Lys Ile Ser Arg Leu Ala Ser Gln Thr
355   360   365   Trp Thr Ala   370

```
L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:177 M:252 E: No. of Seq. differs, <211>LENGTH:Input:371 Found:352 SEQ:2
L:236 M:252 E: No. of Seq. differs, <211>LENGTH:Input:97 Found:80 SEQ:4
L:256 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:13
L:256 M:252 E: No. of Seq. differs, <211>LENGTH:Input:849 Found:720 SEQ:5
L:280 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:13
L:280 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1089 Found:960 SEQ:6
```